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Estimation of the secondary structure and conformation of bovine lens crystallins by infrared spectroscopy: quantitative analysis and resolution by Fourier self-deconvolution and curve fit.

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The secondary structure of six bovine lens protein fractions (two alpha, three beta and one gamma-crystallin) are examined in solution and in solid forms for the first time using FTIR spectroscopy. Films of the nuclear and cortical regions of the bovine lens are also examined. The structure is quantitatively estimated from the vibrational analysis of the resolution-enhanced amide-I profile achieved by Fourier self-deconvolution and linear least-squares curve-fit algorithm. All the protein fractions fold predominantly in a beta-pleated sheet structure with little or no alpha-helical domains in solution or in lyophilized solid form. These proteins also retain their predominant beta-sheet conformation in the cellular phospholipid environment of the lens, in conformity with the structure obtained for all the mammalian species examined to date. Despite structural homology, vibrational data indicate subtle structural differences within each class of the crystallins probably due to presence of several minor substructures/subconformations. Substantial high amounts of turns (approx. 40%) observed in the beta-fractions may have a fundamental implication in stabilizing the tertiary structure of the uniquely folded-proteins vital for the transparency of the lens. These proteins in solid KBr-matrix undergo a major structural change, induced primarily by ionic interactions which refold them in a helical conformation. IR spectroscopy together with band-narrowing procedures has proven to be an effective tool to obtain structural information of proteins in solution, as solid substrates or in a complex biological tissue, such as ocular lens.

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